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## **A comparison of faecal microbial populations of South African Windsnyer-type indigenous pigs (SAWIP) and Large White x Landrace (LW x LR) crosses fed diets containing ensiled maize cobs**

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DOI: <https://doi.org/10.1093/femsle/fnv100>

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ZORA URL: <https://doi.org/10.5167/uzh-122126>

Journal Article

Published Version

Originally published at:

Kanengoni, A; Chimonyo, M; Tasara, Taurai; Chimonyo, P; Chapwanya, A; Ndimba, B; Dzama, K (2015). A comparison of faecal microbial populations of South African Windsnyer-type indigenous pigs (SAWIP) and Large White x Landrace (LW x LR) crosses fed diets containing ensiled maize cobs. *FEMS Microbiology Letters*, 362(13):fnv100.

DOI: <https://doi.org/10.1093/femsle/fnv100>

## RESEARCH LETTER – Taxonomy &amp; Systematics

# A comparison of faecal microbial populations of South African Windsnyer-type indigenous pigs (SAWIPs) and Large White × Landrace (LW × LR) crosses fed diets containing ensiled maize cobs

Arnold T. Kanengoni<sup>1,8,\*</sup>, Michael Chimonyo<sup>2</sup>, Taurai Tasara<sup>3</sup>, Paul Cormican<sup>4</sup>, Aspinas Chapwanya<sup>5</sup>, Bongani K. Ndimba<sup>6,7</sup> and Kennedy Dzama<sup>8</sup>

<sup>1</sup>Agricultural Research Council-Animal Production Institute, Private Bag X2, Irene, 0062, South Africa,

<sup>2</sup>Discipline of Animal & Poultry Science, University of KwaZulu-Natal, Private Bag X01, Scottsville, Pietermaritzburg, 3209, South Africa, <sup>3</sup>Institute for Food Safety and Hygiene, Vetsuisse Faculty University of Zurich, Switzerland, <sup>4</sup>Animal & Grassland Research and Innovation Centre, Teagasc, Grange, Co. Meath, Ireland, <sup>5</sup>Ross University School of Veterinary Medicine, Department of Clinical Sciences, Box 34, Basseterre, St Kitts and Nevis, <sup>6</sup>Agricultural Research Council, Proteomics Research and Services Unit, Helshoogte Road, Infruitech. Nietvorbij Institute, Stellenbosch 7599, South Africa, <sup>7</sup>Department of Biotechnology, University of the Western Cape, Private Bag X17, Bellville, Cape Town, 7535, South Africa and <sup>8</sup>Department of Animal Sciences, Stellenbosch University, Private Bag X1, Matieland, 7602, South Africa

\*Corresponding author: Agricultural Research Council, Private Bag X2, Irene, 0062, South Africa. Tel: +27126729355; Fax: +27126651605;

E-mail: [Arnoldk@arc.agric.za](mailto:Arnoldk@arc.agric.za)

**One sentence summary:** A comparison of faecal microbial populations was carried out to explain differences in digestion of high-fibre diets in South African Windsnyer-type indigenous pigs and Large White × Landrace crosses.

Editor: Abelardo Margolles

## ABSTRACT

Faecal microbial communities in South African Windsnyer-type indigenous pigs (SAWIPs) and Large White × Landrace (LW × LR) crosses were investigated using high-throughput sequencing of the 16S rDNA genes. The faecal microbial communities in LW × LR crosses and SAWIPs fed control (CON) and high maize cob (HMC) diets were evaluated through parallel sequencing of 16S rDNA genes. *Butyrivibrio*, *Faecalibacterium* and *Desulfovibrio*, although present in LW × LR pigs, were absent from the SAWIP microbial community. *Bacteroides*, *Succiniclaticum*, *Peptococcus* and *Akkermansia* were found in SAWIPs but not in LW × LR crosses. The ratios of *Bacteroidia* to *Clostridia* on the CON and HMC diets were similar (0.37 versus 0.39) in SAWIPs but different (0.24 versus 0.1) in LW × LR crosses. The faecal microbial profiles determined were different between the LW × LR and SAWIP breeds but not between pigs fed the CON and HMC diets. The composition of faecal bacterial communities in SAWIPs was determined for the first time. The differences in microbial communities detected may explain the enhanced ability of SAWIPs to digest fibrous diets compared with the LW × LR crosses.

**Keywords:** agriculture; fermentation; genomics; intestinal microbiology; metagenomics

Received: 9 May 2015; Accepted: 15 June 2015

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## INTRODUCTION

Pig production faces the challenge of effectively utilizing fibrous feeds that are readily available (Montagne et al. 2012; Urriola and Stein 2012). In South Africa, for example, maize cobs are a cheap feed ingredient with potential for greater exploitation in pig diets. We recently reported that South African Windsnyer-type indigenous pigs (SAWIPs) digested and utilized diets containing maize cobs better than the Large White  $\times$  Landrace crossbred (LW  $\times$  LR) pigs (Kanengoni et al. 2014, 2015). This hardy breed plays an important role in the rural populations in Southern Africa in that it thrives on high-fibre diets and its characterization is critical in alleviating poverty in resource-poor communities. There has been little research investigating the effect of maize cobs on the dynamics of intestinal microbial communities in grower pigs. The microbes' metabolic processes have a direct influence on the host's gut health and nutrient availability, and this should be considered when formulating diets with unconventional ingredients. Culture-dependent methods are inadequate to elucidate microbial profiles in the hindgut since only 1% of intestinal microbes are culturable (Hugenholtz, Goebel and Pace 1998). Molecular techniques are therefore key to unravelling the complex intestinal microbial communities in humans and animals (O'Flaherty and Klaenhammer 2010; Kau et al. 2011; Gravitz 2012). We hypothesized that the SAWIP intestinal microbiota allows utilization of fibrous diets more efficiently compared with those of Large White crosses. The objective of this study was to evaluate the influence of breed and diet on the faecal microbiome in commercial and indigenous South African breeds fed diets containing ensiled maize cobs using high-throughput sequencing of the 16S rDNA genes.

## MATERIALS AND METHODS

### Animals, diets, housing and experimental design

Six LW  $\times$  LR crossbreds and five SAWIPs from a group of 16 LW  $\times$  LR pigs and 10 SAWIPs that underwent a growth performance and digestibility study (Kanengoni et al. 2014, 2015) were randomly selected for faecal microbial evaluation. These pigs were the progeny of SAWIP and LW  $\times$  LR sows from the Agricultural Research Council-Irene pig breeding units that were bred naturally and farrowed vaginally. The piglets were weaned at 4 and 5 weeks (for the LW  $\times$  LR crosses and SAWIPs, respectively) and raised indoors on similar diets under the same management system. The sows and piglets were not exposed to antimicrobials during the rearing process. As the SAWIPs and LW  $\times$  LR pigs differ in their mature body weights, the pigs started the trial at a similar level of physiological maturity (0.10 of adult body weight). The concept of physiological age was used previously in experimental animals (Kanengoni et al. 2004; Morel, Lee and Moughan 2006). The SAWIPs weighed  $17 \pm 3.4$  kg at 90 days and the LW  $\times$  LR crossbred pigs weighed  $29 \pm 3.6$  kg at 70 days at the onset of the trial. They were slaughtered at finisher weights ( $58 \pm 8.8$  kg for SAWIPs aged 146 days;  $86 \pm 8.8$  kg for LW  $\times$  LR pigs aged 126 days). During the trial, the pigs were individually housed in environmentally controlled houses (temperature 22–25°C) within pens measuring  $2 \times 1.5$  m (LW  $\times$  LR pigs) and  $1.5 \times 0.9$  m (SAWIPs) per animal. Pigs had been blocked by weight and breed and randomly assigned to control (CON; without maize cobs) and high maize cob (HMC; containing 200 g of ensiled maize cob kg<sup>-1</sup>) diets (Supplementary Table S1). Both diets were formulated to provide 14 MJ kg<sup>-1</sup> of digestible energy (DE), 180 g of crude protein (CP) kg<sup>-1</sup> and 11.6 g of lysine kg<sup>-1</sup> per kg of dry

matter (DM) of feed, which meet and exceed the requirements of growing pigs (NRC, 1998). The pigs were fed daily each morning, and 10% extra feed adjustments were made for animals that finished their daily allocation. The pigs were weighed weekly, and daily feed intake was calculated based on feed offered less leftovers. The feeders were checked and adjusted twice each day to ensure *ad lib* access to fresh feed and minimal wastage. Water was freely available through nipple drinkers. At the end of the growth and digestibility study, the pigs were humanely slaughtered at an abattoir <1 km away. The results of the growth and digestibility study have been reported elsewhere (Kanengoni et al. 2014, 2015). The research was approved by the Animal Ethics Committee of the Agricultural Research Council, Animal Production Institute (ARC-API, Ref: APIEC12/018).

### Sampling, DNA extraction and PCR amplification

Pigs were processed in accordance with routine abattoir procedures including an ante-mortem inspection and 1 h rest prior to slaughter. The animals were electrically stunned and exsanguinated within 10 s of stunning. Post-dehairing and evisceration, faecal samples were collected aseptically from the rectum and immediately frozen at -20°C until processed for DNA isolation. A 250 mg aliquot from each faecal sample was thawed and DNA was extracted using the PowerSoil® DNA Isolation Kit (Mo Bio Laboratories Inc., Carlsbad, CA, USA). The V3 and V4 regions of the 16S rDNA gene in these samples were amplified using the GeneAmp® PCR System 9700 (Applied Biosystems, Foster City, CA, USA). Primers S-D-Bact-0341-b-S-17 (3'-TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCTACGGGNGGCWGCAG-5') and S-D-Bact-0785-a-A-21 (3'-GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGACTACHVGGGTATCTAATCC-5') that include adaptors complementary to Illumina forward, reverse and multiplex sequencing primers were used (Klindworth et al. 2013). PCR amplification was carried out in a total volume of 25  $\mu$ L, which contained DNA (20 ng  $\mu$ L<sup>-1</sup>), primers (200 nM) and DreamTaq Green PCR master Mix (Thermo Scientific, Waltham, MA, USA). The thermocycling conditions applied were as previously described (Don et al. 1991). PCR amplicons were separated on a 1% agarose gel and purified using a Qiaquick PCR purification kit (Qiagen, Alameda, CA, USA). Genomic DNA and PCR amplicons were quantified using a Qubit® 2.0 Fluorometer (Invitrogen, Carlsbad, CA, USA).

### Library preparation and Illumina sequencing

Purified PCR products were used as templates to perform an index PCR. In this step, dual indices and Illumina sequencing adaptors were attached to PCR products using the Nextera XT Kit. The index PCR product purification and multiplexing was done following the Illumina 16S sample preparation guide (16S Sample Preparation Guide, 15044223; Illumina, San Diego, CA, USA). The library was sequenced using the Miseq version 2 platform (Illumina) with 300 by 300 bp paired-end V3 reagent chemistry (Illumina MS-102-3003) at the Agricultural Research Council Biotechnology Platform in Pretoria, South Africa (ARC-BTP).

### Sequence processing and analysis

A combination of *de novo* and reference-based operational taxonomic unit (OTU) identification was carried out using the open-reference calling method implemented within the Quantitative Insights Into Microbial Ecology (QIIME) software package. A default similarity level of 97% was used to cluster

sequences into individual OTUs, and a single representative sequence from each clustered OTU was used to align to the GreenGenes database (version: gg\_13.5) (Caporaso et al. 2010). Taxonomic classification for each OTU was determined with the Ribosomal Database Project (RDP) Classifier using a minimum confidence cut-off of 0.8. The OTUs with <100 sequences across all samples were excluded from further analysis. Estimates of distance matrices for both alpha and beta diversity calculation and a per-sample summary of OTU representation at various taxonomic levels were also calculated.

### Statistical analysis

A comparison of bacterial species diversity and richness was conducted using rarefaction analysis. Group- and individual animal-based rarefaction curves were calculated. The similarities and dissimilarities between the groups were evaluated by unweighted (Supplementary Fig. S2; based on the presence or absence of taxa) and weighted (Fig. 2; based on relative abundance) UniFrac-based principal co-ordinates analysis. Abundant species were defined at an empirical cut-off of percentage abundance >1%. Comparisons were made with the 95% significance level. The significant differences of taxa (Phylum, Class, Order, Family and Genus) between CON and HMC diets and the two breeds were determined using a modified  $\chi^2$  test which includes a false discovery rate (FDR) determination to obtain a P-value for the null hypothesis.

## RESULTS AND DISCUSSION

In the digestibility study, we reported that apparent total tract digestibility coefficients of crude protein (CP), acid detergent fibre (ADF), hemicellulose and neutral detergent fibre (NDF) in SAWIPs and LW  $\times$  LR pigs fed HMC-based diets were greater ( $P < 0.05$ ) than in the CON group (Kanengoni et al. 2015). We also reported that the SAWIPs had greater ( $P < 0.05$ ) NDF digestibility coefficients than the LW  $\times$  LR crosses although the latter had greater concentrations of total volatile fatty acids (VFAs) ( $P < 0.05$ ) than the SAWIPs. To investigate these observations further, this study sought to evaluate the influence of breed and diet on the faecal microbiota composition and whether these could provide some insights into the differences in digestibility of nutrients between the LW  $\times$  LR and SAWIP breeds.

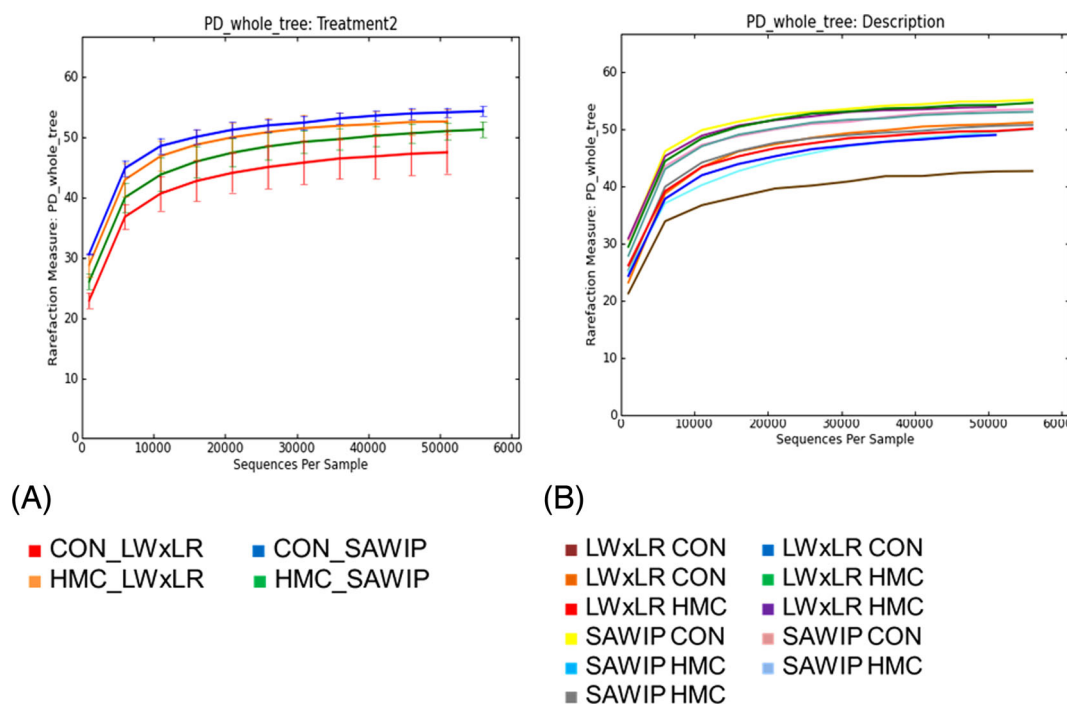
Pigs fed high-fibre diets require 3–5 weeks to adapt to the digestibility of non-starch polysaccharide monomers (Longland et al. 1993). Pigs investigated in the current study were on the same diet for at least 8 weeks, so the intestinal microbes were well adapted and in a stable flux. Pyrosequencing of 16S rDNA amplicons resulted in a total of 280 000 high-quality sequences for SAWIPs and 320 000 for LW  $\times$  LR pigs, with an average of 55 091 sequences (range = 51 000–56 000) per sample. These sequences were classified to OTUs ( $n = 835$ ) and into Bacteria (99.3%) and Archaea (0.7%) kingdoms. The majority of the OTUs detected in these two breeds are similar to those previously described from other pig breeds and other countries (Leser et al. 2002; Upadrashta et al. 2013; Pajarillo et al. 2015). To our knowledge, the 16S rDNA analysis of intestinal microbial communities in the SAWIP breed and similar indigenous breeds in the Southern Africa region has not been done previously. We however also acknowledge that it is difficult to compare studies because of the many variables involved, including differences in faecal sampling methods, DNA extraction and PCR amplification methods, and the variable regions of the 16S rRNA gene analysed among experiments (Wu et al. 2010). In addition, differences in age,

genetics and living environments of individuals across studies may also contribute to the development of the gut microbiota and cannot be ignored (Hooda et al. 2012). Overall 99.3% of the OTUs from the LW  $\times$  LR pigs on the CON diet, 99.6% of the OTUs from LW  $\times$  LR pigs on the HMC diet, 98.85% of the OTUs from SAWIPs on the CON diet and 99.74% of the OTUs from SAWIPs on the HMC diet were assigned to the phylum level. Notably <50% of the OTUs detected in the SAWIPs and LW  $\times$  LR pigs could be assigned to the genus level. Similarly Leser et al. (2002) and Pajarillo et al. (2015) reported that only 17% and 32% of the identified phylotypes in the gastrointestinal tract of Danish and Duroc pigs, respectively, belonged to known species. Lamendella et al. (2011) also reported that unclassified *Firmicutes* and *gammaproteobacteria* were among the top six abundant bacterial groups in pigs. These results are suggestive of a highly complex porcine intestinal microbial community, with the majority of the bacterial genera within this environment yet to be characterized.

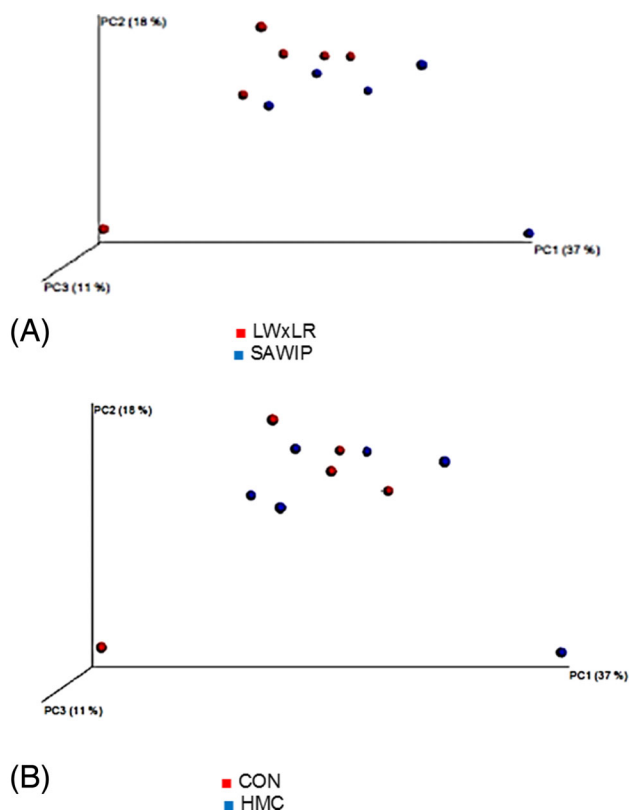
Rarefaction analysis revealed that in all samples the depth of sequence analysis achieved was sufficient to cover the entire species diversity. All curves that were derived reached a plateau, reflecting diminished chances of finding new phylotypes with continued sampling (Fig. 1A and B; Supplementary Fig. S1). A comparison of species diversity in samples grouped based on both breed and diet showed significant differences in the diversity of microbial communities recovered from SAWIPs and LW  $\times$  LR pigs fed the CON diet but not the HMC diet (Fig. 1A). In addition, there were significant faecal bacterial community diversities detected between individual animal-based samples (Fig. 1B). Weighted UniFrac analysis showed that individual pig differences and clustering of the gut microbial communities occurred based on breed (SAWIP; LW  $\times$  LR) but not on diet (CON; HMC) (Fig. 2). However, there were single outliers in both breeds that did not cluster well with the other samples. It has been reported that each individual pig harbours its own specific and unique bacterial composition, even if the animals receive the same diet, stay in the same environment and are siblings (Hill et al. 2005). Although rarefaction estimates showed differences in the number of OTUs identified between breeds, diet and their interactions, there were no overall significant differences in microbial diversity. We presume that due to the small number of pigs used and the presence of outliers in the current study data set, such differences could not be detected (Fig. 2A and B). To confirm these possible differences it is necessary to study a large number of pigs.

Overall the OTUs detected in the LW  $\times$  LR and SAWIP breeds were assigned to 14 phyla, 20 classes, 22 orders, 38 families and 41 genera (Table 1). Notably the genera *Butyrivibrio*, *Faecalibacterium*, *Desulfovibrio* and unidentified *Enterobacteriaceae*, although present in LW  $\times$  LR crosses were absent from SAWIPs. The SAWIP OTUs on the other hand included *Bacteroides*, unidentified RF16, *Succinilasticum*, *Peptococcus*, unidentified *Dethiosulfovibrionaceae*, unidentified *Cerasicoccaceae* and *Akkermansia* that were absent from LW  $\times$  LR pigs. *Faecalibacterium prausnitzii* species are a major representative of the *Firmicutes* phylum, and an acetate-consuming and butyrate-producing gut microbe, and they have been reported to have anti-inflammatory properties (Khan et al. 2012; Hooda et al. 2012). *Butyrivibrio* species are the predominant cellulolytic bacteria in the rumen (Varel, Fryda and Robinson 1984). *Desulfovibrio*, a member of the  $\delta$ -*proteobacteria*, belongs to the group of the sulphate-reducing bacteria that derive their energy from anaerobic respiration, and are able to use a wide variety of inorganic compounds as electron acceptors (Lobo et al. 2007). Members of the *Bacteroides* genus are an important group in terms of pectin degradation, due to their high numbers





**Figure 1.** Rarefaction curves calculated based on phylogenetic diversity (PD) and observed species metrics for Large White  $\times$  Landrace (LW  $\times$  LR) pigs and South African Windsnyer-type indigenous pigs (SAWIPs) fed control (CON) and high maize cob inclusion (HMC) diets based on breed  $\times$  diet interactions (A) and individual animals (B).



**Figure 2.** Weighted UniFrac-based principal co-ordinates plots of (A) the Large White  $\times$  Landrace (LW  $\times$  LR) and South African Windsnyer-type indigenous pig (SAWIP) breeds and (B) the control (CON) and high maize cob inclusion (HMC) diets.

and nutritional versatility (McCarthy, Kotarski and Salyers 1985). *Succiniblasticum ruminis* specializes in fermenting succinate and converting it quantitatively to propionate (Van Gylswyk 1995). *Akkermansia* belongs to the mucus-colonizing bacteria, capable of utilizing mucus as a sole carbon and nitrogen source (Derrien et al. 2004). *Akkermansia* spp. have been suggested as biomarkers for a healthy intestine (Png et al. 2010; Swidsinski et al. 2011). Information on the genotypic or the phenotypic characteristics of the other bacteria is not readily available as far as we could determine. Although the reasons for these differences are not clearly defined, it is known that genotype influences intestinal bacterial diversity in pigs, which might have an impact on their ability to utilize fibrous diets (Varel, Jung and Pond 1988; Pajarillo et al. 2014).

Irrespective of breed, the dominant phyla detected were *Firmicutes* (67.7%), *Bacteroidetes* (14.8%) and *Spirochaetes* (13.5%), whereas *Fibrobacteres*, TM7, *Verrucomicrobia*, *Cyanobacteria*, *Synergistetes*, WPS-2, *Tenericutes*, *Planctomycetes*, *Proteobacteria*, *Actinobacteria* and *Euryarchaeota* were below 1% and accounted for 4.1% of total reads (Table 1). The *Euryarchaeota*, a member of the *Archaea* kingdom, comprised 0.7% of the phyla of which LW  $\times$  LR pigs had 0.5% and the SAWIPs had 0.2%. The LW  $\times$  LR crosses had higher proportions of *Methanospaera* (0.45% versus 0.18%) and *Methanobrevibacter* (0.50% versus 0.16%) than the SAWIPs. Among the *Firmicutes* phylum, *Clostridia* (58.8%) and *Bacilli* (8.4%) were the most dominant classes, whereas the *Bacteroidetes* phylum comprised only the *Bacteroidia* class (14.8%).

Crucially, the SAWIP and LW  $\times$  LR breeds are obese and lean pigs, respectively, and differ in energy metabolism. A relationship between the intestinal tract methanogenic communities and the fatness or leanness of the host has been proposed (Su et al. 2014). Methanogens use hydrogen, formate, methanol and acetate to reduce carbon dioxide to methane, which

**Table 1.** Overall taxonomic classification and proportions (%) of OTUs from LW × LR pigs and SAWIPs independent of diet groupings.

Phylum	Class	Order	Family	Genus	LW × LR (%)	SAWIP (%)
Actinobacteria (0.1%)	Coriobacteriia (0.1%)	Coriobacteriales (0.1%)	Coriobacteriaceae	–	0.10	0.04
				Collinsella	0.05	0.02
Bacteroidetes (14.8%)	Bacteroidia (14.8%)	Bacteroidales (14.8%)	Prevotellaceae	Prevotella	2.37	2.08
			Paraprevotellaceae	CF231	0.23	0.18
				Prevotella	0.42	0.18
				YRC22	1.10	1.50
			BS11	–	0.22	0.66
			Bacteroidaceae	Bacteroides	0.00	0.08
			RF16	–	0.00	0.02
			Porphyromonadaceae	Parabacteroides	0.12	3.94
			p-2534-18B5	–	0.15	0.40
			S24-7	–	5.10	8.74
Cyanobacteria (0.1%)	4C0d-2 (0.1%)	YS2 (0.1%)	–	–	0.05	0.06
Euryarchaeota (0.6%)	Methanobacteria (0.7%)	Methanobacteriales (0.7%)	Methanobacteriaceae	Methanospaera	0.45	0.18
				Methanobrevibacter	0.50	0.16
Fibrobacteres (0.2%)	Fibrobacteria (0.2%)	Fibrobacterales (0.2%)	Fibrobacteraceae	Fibrobacter	0.15	0.28
Firmicutes (67.7%)	Bacilli (8.4%)	Lactobacillales (7.1%)	Streptococcaceae	Streptococcus	1.63	5.58
			Lactobacillaceae	Lactobacillus	4.63	2.58
		Turicibacterales (1.3%)	Turicibacteraceae	Turicibacter	1.12	1.52
	Clostridia (58.8%)	Clostridiales (58.8%)	Lachnospiraceae	Lachnospira	0.95	0.08
				Coprococcus	0.60	0.58
				Other	0.05	0.14
				Epulopiscium	0.00	0.00
				Dorea	0.17	0.30
				Blautia	0.35	0.28
				Shuttleworthia	3.57	0.52
				Roseburia	0.30	0.20
				Butyrivibrio	0.03	0.00
			Ruminococcaceae	Oscillospira	0.88	1.78
				Faecalibacterium	0.03	0.00
				Ruminococcus	2.57	2.70
				–	7.90	12.62
			Clostridiaceae	SMB53	4.92	1.74
				Clostridium	3.55	2.20
				–	22.87	12.90
			Veillonellaceae	Anaerovibrio	0.03	0.02
				Phascolarctobacterium	0.07	0.04
				Succiniclasticum	0.00	0.02
				Megasphaera	0.73	0.08
			Christensenellaceae	–	0.15	1.82
			Mogibacteriaceae	–	0.15	0.20
			Peptostreptococcaceae	–	0.80	0.28
			Peptococcaceae	Peptococcus	0.00	0.04
	Erysipelotrichi (0.5%)	Erysipelotrichales (0.5%)	Erysipelotrichaceae	Catenibacterium	0.03	0.02
				[Eubacterium]	0.03	0.02
				L7A.E11	0.13	0.06
				Bulleidia	0.07	0.08
				p-75-a5	0.23	0.18
Planctomycetes (0.9%)	Planctomycetia (0.9%)	Pirellulales (0.9%)	Pirellulaceae	–	0.55	1.28
Proteobacteria (0.6%)	Betaproteobacteria (0.2%)	Tremblayales (0.2%)	–	–	0.38	0.02
	Deltaproteobacteria (0.0%)	Desulfovibrionales (0.0%)	Desulfovibrionaceae	Desulfovibrio	0.03	0.00
	Epsilonproteobacteria (0.1%)	Campylobacteriales (0.1%)	Campylobacteraceae	Campylobacter	0.03	0.06
	Gammaproteobacteria (0.3%)	Aeromonadales (0.1%)	Succinivibrionaceae	Succinivibrio	0.08	0.06
		Enterobacteriales (0.2%)	Enterobacteriaceae	–	0.30	0.00
Spirochaetes (13.5%)	Spirochaetes (13.5%)	Spirochaetales (13.5%)	Spirochaetaceae	Treponema	12.48	14.66
Synergistetes (0.0%)	Synergistia (0.0%)	Synergistales (0.0%)	Dethiosulfovibrionaceae	–	0.00	0.08
Tenericutes (0.1%)	Mollicutes (0.1%)	RF39 (0.1%)	–	–	0.05	0.12
TM7 (0.1%)	TM7-3 (0.1%)	CW040 (0.1%)	F16	–	0.15	0.06
Other (0.6%)	Other (0.6%)	Other (0.6%)	Other	Other	0.55	0.62
Verrucomicrobia (0.6%)	Opitutae (0.0%)	Cerasicoccales (0.0%)	Cerasicoccaceae	–	0.00	0.04
	Verruco-5 (0.4%)	WCHB1-41 (0.4%)	RFP12	–	0.35	0.42
	Verrucomicrobiae (0.2%)	Verrucomicrobiales (0.2%)	Verrucomicrobiaceae	Akkermansia	0.00	0.46
WPS-2 (0.1%)	– (0.1%)	– (0.1%)	–	–	0.08	0.10

**Table 2.** Relative abundances (%) of faecal bacterial genera in LW × LR and SAWIP breeds fed CON and HMC diets.

Genus	HMC		CON		P-values		
	SAWIP	LW × LR	SAWIP	LW × LR	Breed	Diet	Breed × Diet
<i>Oscillospira</i>	0.9	1.2	3.1	0.5	0.654	0.885	0.02
Unidentified Clostridiaceae	14.1	15.3	11.1	30.5	0.654	0.885	0.534
Unidentified Christensenellaceae	1.9	0.1	1.7	0.2	0.129	0.953	0.534
<i>Prevotella</i>	1.6	4.1	2.9	0.7	0.904	0.885	0.534
SMB53	1.9	3.9	1.4	6.0	0.654	0.885	0.794
Unidentified Bacteroidales	1.6	1.7	1.4	0.4	0.686	0.885	0.794
Unidentified Ruminococcaceae	13.6	8.1	11.2	7.7	0.654	0.885	0.794
<i>Akkermansia</i>	0.8	0.0	0.0	0.0	0.654	0.885	0.794
<i>Parabacteroides</i>	6.5	0.2	0.1	0.03	0.654	0.885	0.794
<i>Streptococcus</i>	6.3	2.5	4.5	0.7	0.654	0.885	0.794
<i>Lactobacillus</i>	0.5	5.3	5.7	4.0	0.713	0.889	0.794
YRC22	1.2	1.9	2.0	0.3	0.819	0.889	0.794
Unidentified Pirellulaceae	1.3	0.4	1.1	0.8	0.654	0.961	0.794
<i>Clostridium</i>	2.8	3.4	1.3	3.6	0.654	0.953	0.823
S24-7	7.7	5.6	10.2	4.6	0.654	0.969	0.865
<i>Turicibacter</i>	1.8	0.7	1.1	1.5	0.800	0.961	0.896
<i>Ruminococcus</i>	2.6	3.1	2.9	2.0	0.904	0.944	0.946
Unidentified Clostridiales	9.0	9.1	8.6	6.2	0.819	0.885	0.946
Unidentified Lachnospiraceae	4.1	4.1	3.2	3.9	0.904	0.953	0.984
<i>Treponema</i>	14.4	11.1	15.1	13.9	0.881	0.961	0.984

translates to an energy loss for the animal (Johnson and Johnson 1995; Montery, Groenestein and Hilhorst 2001). The higher proportions of *Methanospira* and *Methanobrevibacter* in the LW × LR pigs than in SAWIPs suggest that the SAWIP breed may retain more energy. Similarly Landrace pigs exhibited significantly more methanogen diversity than Erhualian pigs (Luo et al. 2012). Erhualian pigs are Chinese indigenous pigs that have not been selected for lean growth and tend to be obese (Luo et al. 2012), making them somewhat similar to the SAWIPs.

Although in this study the abundance of *Firmicutes*, *Bacteroidetes* and *Spirochaetes* between breeds and diets was not significantly different, the ratios of *Bacteroidia* to *Clostridia* in each breed are suggestive of genotype influences. The ratio of *Bacteroidia* to *Clostridia* in SAWIPs on the HMC diet (0.37) was similar to that of those on the CON diet (0.39). In LW × LR pigs fed the HMC diet, the ratio of *Bacteroidia* to *Clostridia* was higher than that of those fed the CON diet (0.24 versus 0.1). Feeding the HMC diet did not result in significant differences in proportions of any bacterial taxa in either the LW × LR pigs or SAWIPs compared with pigs fed the CON diet. Consistent with our observations, other researchers have previously also reported no increase in cellulolytic bacteria in sows fed a 20% maize cob diet (Varel and Pond 1985). Table 2 shows the differences in the abundance of the genera between the breeds and the diets. There was a breed × diet interaction ( $P < 0.05$ ) for the *Oscillospira* genus, which increased in LW × LR pigs as the diet changed from CON to HMC while it decreased in SAWIPs. *Verrucomicrobia opitutae* was detected only in SAWIPs on the HMC diet. There were no differences in breed, diet and breed × diet interactions in the other families. We previously reported that the LW × LR crosses consumed more feed weight wise and per metabolic body weight ( $BW^{0.75}$ ) than SAWIPs at the finisher stage ( $P < 0.05$ ) (Kanengoni et al. 2014). The observed differences in proportions of microbes between the two breeds could be due to different amounts of substrate passing through the gut. However, it could equally be due to the type of substrate. Hooda et al. (2012) proposed that gut

microbial communities will shift due to substrate preference or metabolic cross-feeding.

The functional capabilities of the genus *Oscillospira* have not been determined, but it is likely that it plays a role in fibre fermentation due to its presence in numerous rumen systems and its greater abundance in hosts that are fed fresh forage (Mackie et al. 2003). The phylum *Verrucomicrobia* has a widespread distribution, and is known to be one of the most common and diverse phyla in soil, aquatic habitats and in the gut of eukaryotes (Lee et al. 2009; Kielak et al. 2010). However, since members of this phylum have been difficult to culture, studies on understanding its role have been limited (Kielak et al. 2010). Some members of the *Verrucomicrobia* phylum have been reported to oxidize methane as a sole source of carbon and energy, making them the only known aerobic methanotrophs outside the *Proteobacteria*, and the only extreme acidophilic methanotrophs known (Dunfield et al. 2007; Islam et al. 2008). A related bacterium, strain VeGlc2 of the order *Verrucomicrobiales*, was shown to ferment glucose to acetate, propionate, succinate and CO<sub>2</sub> through the Embden–Meyerhof–Parnas pathway (Janssen 1998).

## CONCLUSION

In conclusion, 16S rDNA profiling analysis of intestinal microbial communities in the SAWIP breed is presented here for the first time. Analysis of faecal microbial communities in this study revealed differences occurring between the LW × LR and SAWIP breeds but not between the CON and HMC diets. These results suggest that the enhanced ability of the SAWIP to digest fibrous diets in comparison with the LW × LR breed may be a consequence of the differences in their intestinal microbial communities. A greater understanding of the roles of the intestinal microbes in utilization of fibrous diets in the SAWIPs could allow the design of rational and innovative approaches to formulate feeds.

## SUPPLEMENTARY DATA

Supplementary data are available at FEMSLE online.

## ACKNOWLEDGEMENTS

The authors would like to thank the Agricultural Research Council Animal Production Institute (ARC-API) for the funding and use of facilities for the study. Special thanks are also extended to the staff from the Pig Nutrition section for their assistance in data collection, and D. Swanevelder and G. Kamgan Nkuekam from the Agricultural Research Council Biotechnology Platform (ARC-BTP) for 16S rDNA profiling analysis of intestinal microbial communities.

**Conflict of interest.** None declared.

## REFERENCES

- Caporaso JG, Kuczynski J, Stombaugh J, et al. QIIME allows analysis of high-throughput community sequencing data. *Nat Methods* 2010;7:335–6.
- Derrien M, Vaughan EE, Plugge CM, et al. *Akkermansia muciniphila* gen. nov., sp. nov., a human intestinal mucin-degrading bacterium. *Int J Syst Evol Microbiol* 2004;54:1469–76.
- Don RH, Cox PT, Wainwright BJ, et al. Touchdown PCR to circumvent spurious priming during gene amplification. *Nucleic Acids Res* 1991;19:4008.
- Dunfield PF, Yuryev A, Senin P, et al. Methane oxidation by an extremely acidophilic bacterium of the phylum *Verrucomicrobia*. *Nature* 2007;450:879–82.
- Islam T, Jensen S, Reigstad LJ, et al. Methane oxidation at 55°C and pH 2 by a thermoacidophilic bacterium belonging to the *Verrucomicrobia* phylum. *Proc Natl Acad Sci USA* 2008;105:300–4.
- Gravitz L. The critters within: your gut microflora might be aiding and abetting diabetes. *Nature* 2012;485:S12–3.
- Hill JE, Hemmingsen SM, Goldade BG, et al. Comparison of ileum microflora of pigs fed corn-, wheat-, or barley-based diets by chaperonin-60 sequencing and quantitative PCR. *Appl Environ Microbiol* 2005;71:867–75.
- Hooda S, Boler BMV, Sero MCR, et al. 454 Pyrosequencing reveals a shift in fecal microbiota of healthy adult men consuming polydextrose or soluble corn fiber. *J Nutr* 2012;142:1259–65.
- Hugenholtz P, Goebel BM, Pace NR. Impact of culture-independent studies on the emerging phylogenetic view of bacterial diversity. *J Bacteriol* 1998;180:4765–74.
- Janssen PH. Pathway of glucose catabolism by strain VeGlc2, an anaerobe belonging to the *Verrucomicrobiales* lineage of bacterial decent. *Appl Environ Microbiol* 1998;64:4830–3.
- Johnson KA, Johnson DE. Methane emissions from cattle. *J Anim Sci* 1995;73:2483–92.
- Kanengoni AT, Chimonyo M, Ndimba BK, et al. Feed preference, nutrient digestibility and colon volatile fatty acid production in growing South African Windsnyer-type indigenous pigs and Large White × Landrace crosses fed diets containing ensiled maize cobs. *Livestock Sci* 2015;171:28–35.
- Kanengoni AT, Chimonyo M, Erlwanger KH, et al. Growth performance, blood metabolic responses, and carcass characteristics of grower and finisher South African Windsnyer-type indigenous and Large White × Landrace crossbred pigs fed diets containing ensiled corn cobs. *J Anim Sci* 2014;92:5739–48.
- Kanengoni AT, Dzama K, Chimonyo M, et al. Growth performance and carcass traits of Large White, Mukota and their F<sub>1</sub> crosses fed on graded levels of maize cobs. *Anim Sci* 2004;78:61–6.
- Kau AL, Ahern PP, Griffin NW, et al. Human nutrition, the gut microbiome and the immune system. *Nature* 2011;474:327–36.
- Khan MT, Duncan SH, Stams AJM, et al. The gut anaerobe *Faecalibacterium prausnitzii* uses an extracellular electron shuttle to grow at oxic-anoxic interphases. *ISME J* 2012;6:1578–85.
- Kielak A, Rodrigues JLM, Kuramae EE, et al. Phylogenetic and metagenomic analysis of *Verrucomicrobia* in former agricultural grassland soil. *FEMS Microbiol Ecol* 2010;71:23–33.
- Klindworth A, Pruesse E, Schweer T, et al. Evaluation of general 16S ribosomal RNA gene PCR primers for classical and next-generation sequencing-based diversity studies. *Nucleic Acids Res* 2013;41:1.
- Lee K-C, Webb RI, Janssen PH, et al. Phylum *Verrucomicrobia* representatives share a compartmentalized cell plan with members of bacterial phylum *Planctomycetes*. *BMC Microbiol* 2009;9:5.
- Lamendella R, Santo Domingo JW, Ghosh S, et al. Comparative fecal metagenomics unveils unique functional capacity of the swine gut. *BMC Microbiol* 2011;11:103.
- Leser TD, Amenuvor JZ, Jensen TK, et al. Culture-independent analysis of gut bacteria: the pig gastrointestinal tract microbiota revisited. *Appl Environ Microbiol* 2002;68:673–80.
- Lobo SAL, Melo AMP, Carita JN, et al. The anaerobe *Desulfovibrio desulfuricans* ATCC 27774 grows at nearly atmospheric oxygen levels. *FEBS Lett* 2007;581:433–6.
- Longland AC, Low AG, Quelch DB, et al. Adaptation to the digestion of non-starch polysaccharide in growing pigs fed on cereal or semi-purified basal diets. *Br J Nutr* 1993;70:557–66.
- Luo YH, Su Y, Wright ADG, et al. Lean breed Landrace pigs harbor fecal methanogens at higher diversity and density than obese breed Erhualian pigs. *Archaea* 2012;2012:605289.
- Mackie RI, Aminov RI, Hu W, et al. Ecology of uncultivated *Oscillospira* species in the rumen of cattle, sheep, and reindeer as assessed by microscopy and molecular approaches. *Appl Environ Microbiol* 2003;69:6808–15.
- McCarthy RE, Kotarski SF, Salyers AA. Location and characteristics of enzymes involved in the breakdown of polygalacturonic acid by *Bacteroides thetaiotaomicron*. *J Bacteriol* 1985;161:493–9.
- Montagne L, le Floch N, Arturo-Schaan M, et al. Comparative effects of level of dietary fiber and sanitary conditions on the growth and health of weanling pigs. *J Anim Sci* 2012;90:2556–69.
- Monteny GJ, Groenestein CM, Hilhorst MA. Interactions and coupling between emissions of methane and nitrous oxide from animal husbandry. *Nutr Cycl Agroecosyst* 2001;60:123–32.
- Morel PCH, Lee TS, Moughan PJ. Effect of feeding level, live weight and genotype on the apparent faecal digestibility of energy and organic matter in the growing pig. *Anim Feed Sci Technol* 2006;126:63–74.
- NRC. *Nutrient Requirements of Swine*, 10th ed. Washington, DC: National Academy Press, 1998.
- O'Flaherty S, Klaenhammer TR. The role and potential of probiotic bacteria in the gut, and the communication between gut microflora and gut/host. *Int Dairy J* 2010;20:262–8.
- Pajarillo EAB, Chae J-P, Balolong MP, et al. Characterization of the fecal microbial communities of Duroc pigs using 16S



- rRNA gene pyrosequencing. *Asian Australas J Anim Sci* 2015;**4**: 584–91.
- Pajarillo EAB, Chae J-P, Balolong MP, et al. Pyrosequencing-based analysis of fecal microbial communities in three purebred pig lines. *J Microbiol* 2014;**52**:646–51.
- Png CW, Linden SK, Gilshenan KS, et al. Mucolytic bacteria with increased prevalence in IBD mucosa augment in vitro utilization of mucin by other bacteria. *Am J Gastroenterol* 2010;**105**:2420–8.
- Su Y, Bian G, Zhu Z, et al. Early methanogenic colonisation in the faeces of Meishan and Yorkshire piglets as determined by pyrosequencing analysis. *Archaea* 2014;**2014**: 547908.
- Swidsinski A, Dorffle Y, Loening-Baucke V, et al. Acute appendicitis is characterised by local invasion with *Fusobacterium nucleatum/necrophorum*. *Gut* 2011;**60**: 34–40.
- Upadrashta A, O'Sullivan L, O'Sullivan O, et al. The effect of dietary supplementation with spent cider yeast on the swine distal gut microbiome. *PLoS One* 2013;**8**:e75714.
- Urriola PE, Stein HH. Comparative digestibility of energy and nutrients in fibrous feed ingredients fed to Meishan and Yorkshire pigs. *J Anim Sci* 2012;**90**:802–12.
- Van Gylswyk NO. *Succiniclasticum ruminis* gen. Nov., sp. Nov., a ruminal bacterium converting succinate to propionate as the sole energy-yielding mechanism. *Int J Syst Bacteriol* 1995;**45**:297–300.
- Varel VH, Fryda SJ, Robinson IM. Cellulolytic bacteria from pig large intestine. *Appl Environ Microbiol* 1984;**47**:219–21.
- Varel VH, Jung HG, Pond WG. Effects of dietary fiber of young adult genetically lean, obese and contemporary pigs: rate of passage, digestibility and microbiological data. *J Anim Sci* 1988;**66**:707–12.
- Varel VH, Pond WG. Enumeration and activity of cellulolytic bacteria from gestating swine fed various levels of dietary fiber. *Appl Environ Microbiol* 1985;**49**:858–62.
- Wu GD, Lewis JD, Hoffmann C, et al. Sampling and pyrosequencing methods for characterizing bacterial communities in the human gut using 16S sequence tags. *BMC Microbiol* 2010;**10**:206.